## JUN 0 1 2006

"Replacement Sheet"
The Human E3α Ubiquitin Ligase Family
Han et al. - Appl. No. 10/758,672
Atty Docket: 01017/35966B
Fig. 1A (Page 1 of 23)

6 mouse_E3αII DCGDTEAWKE GPYCQKHKLS 4 human_E3αII DCGDTEAWKE GPYCQKHELN 15 mouse_E3αI DCGDTEAWKT GPFCVDHEPG 2 human_E3αI DCGDTEAWKT GPFCVNHEPG Consensus DCGDTEAWK. GP. C HE	6 mouse_E3αII GRVFKVGEPT YSCRDCAVDP 4 human_E3αII GRVFKVGEPT YSCRDCAVDP 15 mouse_E3αI GRVFKSGETT YSCRDCAI DP 2 human_E3αI GRVFKSGETT YSCRDCAI DP Consensus GRVFK.GE.T YSCRDCA.DP	6 mouse_E3αll YCRGPNPFPQ KEDTLAQHIL 4 human_E3αll YCRGPNPFPQ KEDMLAQHVL 15 mouse_E3αl YFAEMDPDLE KQEESVQMSI 2 human_E3αl YFAEMDPDLE KQEESVQMSI Consensus YPKQ	6 mouse_E3αII MASEMEPEVQ AID-RSLLEC 4 human_E3αII MASELEPEVQ AID-RSLLEC 15 mouse_E3αI MADEEMDGAE RMDVSPEPPL 2 human_E3αI MADEEAGGTE RMEISAELPQ Consensus MA. E
GPYCQKHKLS SSEVVEEEDP LVHLSEDVI A RTYNI FAI MFGPYCQKHELN TSEIEEEEEDP LVHLSEDVI A RTYNI FAI TFGPFCVDHEPG RAGTTKESLH - CPLNEEVI A QARRI FPSVIGPFCVNHEPG RAGTI KENSR - CPLNEEVI V QARKI FPSVIGP. C HE F	TCVLCMECFL GSI HRDHRYR MTTSGGGGFC TCVLCMECFL GSI HRDHRYR MTTSGGGGFC TCVLCMDCFQ SSVHKNHRYK MHTSTGGGFC TCVLCMDCFQ DSVHKNHRYK MHTSTGGGFC TCVLCMCF, S. H HRY, M TS. GGGFC	LGPMEWYICA EDPALGFPKL EQANKPSHLC LGPMEWYLCG EDPAFGFPKL EQANKPSHLC LTPLEWYLFG EDPDICLEKL KHSG-AFQLC FTPLEWYLFG EDPDICLEKL KHSG-AFQLC L. P. EWYL. G EDPKLLC	SAEEI AGRWL QATDLNREVY QHLAHCVPKI SAEEI AGKWL QATDLTREVY QHLAHYVPKI APQRPASWWD QQVDFYTAFL HHLAQLVPEI TPQRLASWWD QQVDFYTAFL HHLAQLVPEI
199 199 198 198 200	149 149 149 149 149	99 99 99 99	49 50 50

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	•	
6 4 15 2	15	15
mous e_E3aII huma n_E3aII mous e_E3aI huma n_E3aI Cons ens us	mous e_E3αII huma n_E3αII mous e_E3αI huma n_E3αI Cons ens us	mous e_E3aII huma n_E3aII mous e_E3aI huma n_E3aI Cons ens us
KVQVMHSSVA AHQNFGLKAL SWLGSVIGYS DGLRRILCQV KVQVMHSSIV AHQNFGLKLL SWLGSIIGYS DGLRRILCQV HVEVLHSVVM AHQKFALRLG SWMNKIMSYS SDFRQIFCQA HVEVLHSEIM AHQKFALRLG SWMNKIMSYS SDFRQIFCQA V.V.HS AHQ.F.L.L. SWIYSR.I.CO	VNCTQKEAI G FATTVDRDGR RPVRYGDFQY CDQAKTVI VR VNCTQKEAI G FATTVDRDGR RSVRYGDFQY CEQAKSVI VR LDCELAEAQL HTTAI DKEGR RAVKAGVYAT CQEAKEDI KS LDCELAEAQL HTTAI DKEGR RAVKAGAYAA CQEAKEDI KS C EA T D GR R. V G C AK I	RYAVDILTWE KESELPEDLE VAEKSDTYYC MLFNDEVHTY EQVIYTLQKA RYAVEILTWE KESELPADLE MVEKSDTYYC MLFNDEVHTY EQVIYTLQKA KYIVEMTIWE EEKELPPELQ IREKNERYYC VLFNDEHHSY DHVIYSLQRA KYVVEMTIWE EEKELPPELQ IREKNERYYC VLFNDEHHSY DHVIYSLQRA .Y.VEWE .E.ELPLEKYYC .LFNDE.H.YVIY.LQ.A
AHQNFGLKAL AHQNFGLKLL HQKFALRLG AHQKFALRLG AHQKFALRLG	FATTVDRDGR RPVRYGDFQY FATTVDRDGR RSVRYGDFQY HTTAI DKEGR RAVKAGVYAT HTTAI DKEGR RAVKAGAYAA TDGR R.VG	KESELPEDLE KESELPADLE EKELPPELQ I
SWLGSVI GYS SWLGSI I GYS SWWNKI MSYS SWWNKI MSYS	RPVRYGDFQY RSVRYGDFQY RAVKAGVYAT RAVKAGAYAA R. V G	VAEKSDTYYC MVEKSDTYYC I REKNERYYC I REKNERYYC
DGLRRI LCQV DGLRRI LCQV SDFRQI FCQA SDFRQI FCQA	CDQAKTVI VR CE QAKS VI VR CQE AKEDI KS CQE AKEDI KS C. AK. I.	ML F NDE VHT Y ML F NDE HHS Y VL F NDE HHS Y L F NDE HHS Y . L F NDE . H. Y
GL QE GP DGEN GL QE GP DGEN CL VEE PGS EN CLREEP DS EN	VR NTSRQTK-PL VR NTSRQTK-PL KS HSENVSQHPL KS HSENVSQHPLPL	EQVI YTL QKA EQVI YTL QKA DHVI YSL QRA DHVI YSL QRA VI Y. LQ. A
348 348 348	298 298 298 298 298 300	249 249 248 248 250

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6 m 4 h 15 m 2 h	15 m 2 h
mous e_E3aII huma n_E3aII mous e_E3aI huma n_E3aI Cons ens us	mous e_E3αII huma n_E3αII mous e_E3αI huma n_E3αI Cons ens us
LQRDF MEDDH ERAVSVTALS LQRDF MEDDH ERAVSVTALS LQKEYI SDDH ERSI SI TALS LQKEYI SDDH DRSI SI TALS LQKEYI SDDH ER S. TALS	SSLVDRLMLN DSKLWKGARS SSLVDRLMLS DSKLWKGARS PCLI SRLMLW DAKLYKGARK PCLI SRLMLW DAKLYKGARK
LQRDFMEDDH ERAVSVTALS VQFFTAPTLA RMLITEENLM TLQRDFMEDDH ERAVSVTALS VQFFTAPTLA RMLITEENLM SLQKEYI SDDH ERSI SI TALS VQMLTVPTLA RHLI EEQNVI SLQKEYI SDDH DRSI SI TALS VQMFTVPTLA RHLI EEQNVI SLQKEYI SDDH DRSI SI TALS VQNFTVPTLA RHLI EEQNVI SLQK DDH ER S. TALS VQ. FT. PTLA R I I F N	SSLVDRLMLN DSKLWKGARS VYHQLFMSSL LMDLKYKKLF A SSLVDRLMLS DSKLWKGARS VYHQLFMSSL LMDLKYKKLF A PCLISRLMLW DAKLYKGARK ILHELIFSSF FMEMEYKKLF A PCLISRLMLW DAKLYKGARK ILHELIFSSF FMEMEYKKLF ALRLML D.KL.KGARH.LSSMYKKLF A
TVI I KAFMDH SI I I KTFMDH SVI TETLLEV SVI TETLLEV	ALRFAKNYRQ AVRFAKNYQQ AMEFVKYYKQ AMEFVKYYKQ AF.K.Y.Q
448 448 448 448	398 398 398 398 400

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	0 (- ugc + 01	23)	
15	15	6 4 15 2	SEQ
mous e_E3αII huma n_E3αII mous e_E3αI huma n_E3αI Cons ens us	mous e_E3aII human_E3aII mous e_E3aI human_E3aI Cons ens us	mous e_E3αII huma n_E3αII mous e_E3αI huma n_E3αI Cons ens us	SEQ I D NO:
SMVQDWCALD EKVLIEAYKK SMWQDWCASD EKVLIEAYKK LMFQEWCACD EDLLLVAYKE LMFQEWCACD EELLLVAYKE . M Q. WCA. D E L AYK.	KFLQGFDAFL ELLKCMQGMD KFLEGFDAFL ELLKCMQGMD QFLEGFRSFL KILTCMQGME QFLEGFRSFL KILTCMQGME .FLEGFFLL.CMQGM	LKHRDAQGRF LRHRDAQGRF LPEYLDRNN- LPEYLDRNN- L	
	ELLKCMQGMD ELLKCMQGMD KILTCMQGME KILTCMQGME	QFERYTALQA FKFRRVQSLI QFERYTALQA FKFRRVQSLI KFN- FQGYSQ DKLGRVYAVI KFN- FQGYSQ DKLGRVYAVI . F K RVI	
CLAVLTOCHG GFTDGECCLAVLMQCHG GYTDGECCHKAVMRCST NFMSSTKCHKAVMRCST SFISSSK	PI TRQVGQHI PI TRQVGQHI EI RRQVGQHI EI RRQVGQHI	FKFRRVQSLI FKFRRVQSLI DKLGRVYAVI DKLGRVYAVI . K RV I	
CLAVLTOCHG GFTDGEQPIT LSICGHSVET CLAVLMQCHG GYTDGEQPIT LSICGHSVET CHKAVMRCST NFMSSTKTV- VQLCGHSLET CHKAVMRCST SFISSSKTV- VQSCGHSLET CM.CF	EMEPEWEAAF TLOMKLTHVI EMEPEWEAAF TLOMKLTHVI EVDPDWEAAI AI QMQLKNI L EVDPDWEAAI AI QMQLKNI L E. P. WEAA QM L	LDL KYVLI SK CDL KYI LI SK CDL KYI LI SK CDL KYI LI SK	
	TLQWKLTHVI TLQWKLTHVI AI QWQLKNI L AI QWQLKNI L QM L	LDLKYVLISK PTEWSDELRQ LDLKYVLISK PTEWSDELRQ CDLKYILISK PVIWTERLRA CDLKYILISK PTIWTERLRM . DLKY. LISK PT. W LR.	
598 598 595 595	548 548 546 546 546	498 498 496 496 500	

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6 4 15 2	15	15
mous e_E3αII huma n_E3αII mous e_E3αI huma n_E3αI Cons ens us	mous e_E3αII huma n_E3αII mous e_E3αI huma n_E3αI Cons ens us	mous e_E3aII huma n_E3aII mous e_E3aI huma n_E3aI Cons ens us
QTGVSMMDPN HFLM MLSRF ELYQLFSTPD YGKRFSSE QTGVSMMDPN HFLM MLSRF ELYQIFSTPD YGKRFSSE QI GASI MDPN KFLLLVLQRY ELTDA FNKTI ST-QI GASLMDPN KFLLLVLQRY ELAEA FNKTI ST-Q. G. S. MDPN . FLL.R. ELT K	IEHPLRCLVL CAQVHAGMWR IEHPLRCLVL CAQVHAGMWR VEYPLRCLVL VAQVVAEMWR VEYPLRCLVL VAQVVAEMWR .E.PLRCLVL .AQV. A. MWR	IRYCVSQEKV SIHLPISRLL AGLHVLLSKS EVAYKFPE IYCVSQEKV SIHLPVSRLL AGLHVLLSKS EVAYKFPEL KSYKVSEDLV SIHLPLSRTL AGLHVRLSRL GAISRLHE KSYRVSEDLV SIHLPLSRTL AGLHVRLSRL GAVSRLHE Y.VSV SIHLP.SR.L AGLHV.LSE
QTGVSMWDPN HFLM MLSRF ELYQLFSTPD YGKRFSSEVT HKDVVQQNNT QTGVSMWDPN HFLM MLSRF ELYQIFSTPD YGKRFSSEIT HKDVVQQNNT QI GASI MDPN KFLLLVLQRY ELTDA FNKTI STK DQDLI KQYNT QI GASLMDPN KFLLLVLQRY ELAEA FNKTI STK DQDLI KQYNT Q. G. S. MDPN . FLL.R. ELT. K	RNGFSLVNQI YYYHNVKCRR EMFDKDIVML RNGFSLVNQI YYYHNVKCRR EMFDKDVVML RNGLSLISQV FYYQDVKCRE EMYDKDIIML RNGLSLISQV FYYQDVKCRE EMYDKDIIML RNG. SLQYYVKCR. EM. DKDI.ML	IRYCVSQEKV SIHLPISRLL AGLHVLLSKS EVAYKFPELL PLSELSPPMLIYCVSQEKV SIHLPVSRLL AGLHVLLSKS EVAYKFPELL PLSELSPPMLKSYKVSEDLV SIHLPLSRTL AGLHVRLSRL GAISRLHEFV PFDSFQVEVLKSYRVSEDLV SIHLPLSRTL AGLHVRLSRL GAVSRLHEFV SFEDFQVEVLY.VSV SIHLP.SR.L AGLHV.LSEPL
T HKDVVQQNNT  K DQDLI KQYNT  K DQDLI KQYNT	EMFDKDI VML EMFDKDVVML EMYDKDI I ML EMYDKDI I ML	ELL PLSELSPPML FV PFDSFQVEVL FV SFEDFQVEVL . P L
748 748 738 738	698 698 695 695	648 648 645 645

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15	2 1 5	6 4 15 2
mous e_E3aII huma n_E3aII mous e_E3aI huma n_E3aI Cons ens us	mous e_E3αII huma n_E3αII mous e_E3αI huma n_E3αI Cons ens us	mous e_E3αII huma n_E3αII mous e_E3αI huma n_E3αI Cons ens us
SRAEQSKAEE AQRKLKRENK EDTALPPPAL SRAEQSKAEE AQRKLKRQNR EDTALPPPVL SKTQHSKAEH MQKKRRKQEN KDEALPPPPP SKTQHSKAEH MQKKRRKQEN KDEALPPPPP SSKAEQ.KQD.ALPPP.	SLPEDENKET GMESVIESVA HFKKPGLTGR SLPEDENKET GMESVIEAVA HFKKPGLTGR NLPENENNET GLENVINKVA TFKKPGVSGH NLPENENNET GLENVINKVA TFKKPGVSGH . LPE. EN. ET G. E. VI VA . FKKPG G.	LIEEMLYLII MLVGERFNPG VGQVAATDEI LIEEMLYLII MLVGERFSPG VGQVNATDEI LIEEMLQVLI YIVGERYVPG VGNVTREEVI LIEEMLQVLI YIVGERYVPG VGNVTKEEVT LIEEMLIVGERPG VG.VI
	HFKKPGLTGR HFKKPGLTGR TFKKPGVSGH TFKKPGVSGH . FKKPG G.	
EDTALPPPAL PPFCPLFASL VEDTALPPPVL PPFCPLFASL VEDTALPPPPP PEFCPAFSKV VEDEALPPPPP PEFCPAFSKV I.D. ALPPP. P. FCP. F V	GMYELKPECA GMYELKPECA GVYELKDESL GVYELKDESL G. YELK. E	KREI I HQLSI KREI I HQLSI MREI THLLCI MREI I HLLCI . REI I H. L. I
VNI LQCDVML VNI LQSDVML I NLLNCDI MM VN. L. CDVM	HFKKPGLTGR GMYELKPECA KEFNLYFYHF HFKKPGLTGR GMYELKPECA KEFNLYFYHF TFKKPGVSGH GVYELKDESL KDFNMYFYHY TFKKPGVSGH GVYELKDESL KDFNMYFYHY .FKKPGG. G.YELK.E K.FN.YFYH.	KPMAHSELVK KPMAHSELVK EPMPHSAI AR EPMPHSAI AK . PM HS K
898 888 888 898	848 848 838 838 850	798 798 788 788 800

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SEQ ID NO:

	rig. 10 (Page / of 23)	
6 4 15 2	15	6 15 2
mous e_E3aII huma n_E3aI mous e_E3aI huma n_E3aI Cons ens us	mous e_E3αII huma n_E3αII mous e_E3αI huma n_E3αI Cons ens us	mous e_E3αII huma n_E3αII mous e_E3αI huma n_E3αI Cons ens us
IKKIRECS SSSPVAEAEG VKKMRESS PTSPVAETEG VKRLREKSCL VVATTSGLEC VKRLREKSCL IVATTSGSES VKRECE.	TFTFTQKI SK PGDAPHNSPS TFTFTQKI SK PGEAPKNSPS AFDFYHKASR LGSSAMNAQN TFDFYHKASR LGSSAMNI QM TF.FK.SGN	YI MGTI LQWA CI MGTI LQWA YI LRTI FERA YI LRTVFERA YI TI A
IKKIRECS SSSPVAEAEG TIMEESSRDK VKKMRESS PTSPVAETEG TIMEESSRDK VKRLREKSCL VVATTSGLEC IKSEEITHDK VKRLREKSCL IVATTSGSES IKNDEITHDK VKRECEEEDK	_	YI MGTI LQWA VEHHGSAWSE SMLQRVLHLI CI MGTI LQWA VEHNGYAWSE SMLQRVLHLI YI LRTI FERA VDTESNLWTE GMLQMAFHI L YI LRTVFERA I DTDSNLWTE GMLQMAFHI L YI TI A V W. E . MLQ H
	I LAMLETLQN I LAMLETLQN I QMLLERLKG LLEKLKG	
DKAERKRKAE DKAERKRKAE EKAERKRKAE EKAERKRKAE KAERKRKAE	APSLEAHKDM I RWLLKMFNA APYLEVHKDM I RW LKTFNA I PQLEGQKDM I TW LQMFDT I PQLEGQKDM I TW LQMFDT . P. LE KDM I . W L. MF	GMAL QEEKHH GMAL QEEKQH ALGLLEEKQQ ALGLLEEKQQL. EEKQ.
I ARLRREKI M 1046 I ARLRREKI M 1046 AARLHRQKI M 1037 AARLHRQKI M 1034 . ARL. R. KI M 1050	KDM I RWLLKMFNA KDM I RW LKTFNA KDM I TW LQMFDT KDM I TW LQMFDT KDM I . W L. MF	LENAVEGHVQ LENVTEEHVV LQKAPEEEV- LQKAPEEEV- L A. EE. V.
1046 1046 1037 1034 1050	998 998 987 984 1000	948 948 937 937 937 950

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6 4 15 2	1 4 4 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2	6 4 15 2
mous e_E3\all human_E3\all II mous e_E3\all I human_E3\all I consensus	mous e_E3αII huma n_E3αII mous e_E3αI huma n_E3α Cons ens us	mous e_E3αII huma n_E3αII mous e_E3αI huma n_E3αI Cons ens us
AD- PEKYDPL FMHPDLSCGT QD- PEKYDPL FMDPDLSCGT DHLGETLDPL FMDPDLAHGT ELSGEALDPL FMDPDLAYGT	AQTQVPEPRQ FVTCILCQEE TQTQVPEQRQ FVTCILCQEE KRGPAVTEKE VLTCILCQEE KRGPSVTEKE VLTCILCQEE	AQMS EMQRHF I DENKELFQC AQMS EMQRHF I DENKELFQC AQMS ALQKNF I ETHKLMYDN AQMS ALQKNF I ETHKLMYDN AQMS Q F I K
AD-PEKYDPL FMHPDLSCGT HTGSCGHVMH AHCWQRYFDS VQAKEQRRQQ 1193 QD-PEKYDPL FMHPDLSCGT HTSSCGHIMH AHCWQRYFDS VQAKEQRRQQ 1193 DHLGETLDPL FMDPDLAHGT YTGSCGHVMH AVCWQKYFEA VQLSSQQ 1184 ELSGEALDPL FMDPDLAYGT YTGSCGHVMH AVCWQKYFEA VQLSSQQ 1181EDPL FM PDLGT .TGSCGHVMH A.CWQ YF VQ	AQTQVPEPRQ FVTCILCQEE QEVTVGSRAM VLAAFVQRST VLSKDRTKTI 1144 TQTQVPEQRQ FVTCILCQEE QEVKVESRAM VLAAFVQRST VLSKNRSKFI 1144 KRGPAVTEKE VLTCILCQEE QEVKLENNAM VLSACVQKST ALTQHRGKPV 1137 KRGPSVTEKE VLTCILCQEE QEVKIENNAM VLSACVQKST ALTQHRGKPI 1134	AQMSEMQRHF I DENKELFQQ TLELDTSASA TLDSSPPV SDAALTALGP 1094 AQMSEMQRHF I DENKELFQQ TLELDASTSA VLDHSPVA SDMTLTALGP 1094 AQMSALQKNF I ETHKLMYDN TSEVTGKEDS I MEEESTSAV SEASRI ALGP 1087 AQMSALQKNF I ETHKLMYDN TSEMPGKEDS I MEEESTPAV SDYSRI ALGP 1084 AQMSQF IK T.ES.P.V SDALGP 1100
VQAKEQRRQQ 1193 VQAKEQRRQQ 1193 VQLSSQQ 1181 VQLSSQQ 1181	VLSKDRTKTI 1144 VLSKNRSKFI 1144 ALTQHRGKPV 1137 ALTQHRGKPI 1134 .LR.K.I 1150	TLDSSPPV SDAALTALGP 1094 VLDHSPVA SDMTLTALGP 1094 I MEEESTSAV SEASRI ALGP 1087 I MEEESTPAV SDYSRI ALGP 1084 S.P.V SDALGP 1100

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15	6 4 15 2	6 4 15 2
mous e_E3αII huma n_E3αII mous e_E3αI huma n_E3αI Cons ens us	mous e_E3αII huma n_E3αII mous e_E3αI huma n_E3αI Cons ens us	mous e_E3αII huma n_E3αII mous e_E3αI huma n_E3αI Cons ens us
FYPRNPYS DS FRPKI PYS ES VQS SVKYS NS VESSI KYS NS	DLAQWTRAVT NLTQW RTI S TLARW QTVL TLARW QTVL . LA. W . TV.	RLRLHTSYDV RLRLHTSYDV RI HVDL-FDL RI HVDL-FDL R D.
FYPRNPYSDS I KEMLTTFGT AAYKVGLKVHFRPKI PYSES I KEMLTTFGT ATYKVGLKVHVQS SVKYSNS I KEMVI LFAT TI YRI GLKVPVESSI KYSNS I KEMVI LFAT TI YRI GLKVPVESSI KYSNS I KEMVI LFAT TI YRI GLKVP	DLAQWTRAVT QQIKVVQMLR RKHNAA-DTS SSEDTEAMNINLTQW RTIS QQIKALQFLR KEESTP-NNA STKNSENVDETLARW QTVL ARISGYNIKH AKGEAPAVPV LFNQGMGDSTTLARW QTVL ARISGYNIRH AKGENP-IPI FFNQGMGDSTLARW QTVL ARISGYNIRH AKGENP-IPI FFNQGMGDSTLARW QTVL ARISGYNIRH AKGENP-IPI FFNQGMGDST	ENGEFLCPLC ECLSNTVI PL ENGEFLCPLC ECLSNTVI PL ESGEYLCPLC KSLCNTVI PI ESGEYLCPLC KSLCNTVI PI E. GE. LCPLC L. NTVI P.
	QQI KVVQMLR RKHNAA- DTS SSEDTEAMNI QQI KALQFLR KEESTP- NNA STKNSENVDE ARI SGYNI KH AKGEAPAVPV LFNQGMGDST ARI SGYNI RH AKGENP- I PI FFNQGMGDST	
PNEGDPRVPI LCWGTCAYTI PNEEDPRVPI MCWGSCAYTI PDELDPRVPM MTW5TCAFTI PDERDPRVPM LTW5TCAFTI P. E. DPRVP W. TCA, TI	• • • • • • • • • • • • • • • • • • • •	L-LPPRSILS L-LPPRNIFN I PLQPQKI NS I PLQPQKI NS
	I PI PEGFRPD LQLPEGFRPD FEFHSI LSFG LEFHSI LSFG	RRLN-FSDQP NRLN-FSDQP ENAEALAQLL ENADALAQLL
1340 1340 1333 1329 1350	1290 1290 1283 1279 1300	1241 1241 1233 1230 1250

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1532 1532 1533 1525 1525	1581 1581 1583 1575 1600	1631 1631 1633 1625
FHYLNGVPAP 1532 FHYLNGVPSP 1532 FHYLLGVAPP 1533 FHYLLGVTPP 1525 FHYLLGVTPP 1525	ENSDIMNSLI ESWCQNSEVK 1581 ENSEIMNSLI ESWCRNSEVK 1581 EYWDTIRPLL QRWCGDPALL 1583 EYWDTVRPLL QRWCADPALL 1575 EDLWC 1600	NQASNFSCPK SGGDKSRAPT 1631 NQASNFSCPK SGGDKSRAPT 1631 NQASHFRCPR SADDERKHPV 1633 NQASHFRCPR SADDERKHPV 1625 NQAS.F.CP. SDP. 1650
MPFLKCSAL MPFLKCSALF TPYLRCAALL TPYLRCAALF		NQASNFSCPK NQASNFSCPK NQASHFRCPR NQASHFRCPR
SALKEAPSGW HLWRSVRAAI MPFLKCSAL SALKEIPSGW HLWRSVRAGI MPFLKCSALF GLTGCGAPGW YLWLSLRNGI TPYLRCAALL GSIGCDIPGW YLWVSLKNGI TPYLRCAALF	LPTNLIHLFQ LPNNLICLFQ LPTNLFLLFQ LPTNLFLLFQ LPTNLFLLFQ	DLPEDYSSLI NLPEDYSSLI ELPEDYSCLL ELPDDYSCLL
LHKTLHQYTG SALKEAPSGW HLWRSVRAAI MPFLKCSAL LYKTLHQYTG SALKEIPSGW HLWRSVRAGI MPFLKCSAL FFVEVSQHTD GLTGCGAPGW YLWLSLRNGI TPYLRCAALI FFAEISQYTS GSIGCDIPGW YLWVSLKNGI TPYLRCAALI	HFEHLCNYLS HFEHLCSYLS EFSALCSYLS EYSALCSYLS . F LCSYLS	SYPRGANKLI RYPRESNKLI RYPRKRNSLI RYPRKRNSLI
LHKTLHQYTG LYKTLHQYTG FFVEVSQHTD FFAEISQYTS	PDLQV-SGTS PDIQV-PGTS EELFANSAEG EELHTNSAEG	RYLNGERGAI RYLEGERDAI KSLKQKSAVV NCLKQKNTVV
6 mouse_E3αII 4 human_E3αII 15 mouse_E3αI 2 human_E3αI Consensus	6 mouse_E3aII 4 human_E3aII 15 mouse_E3aI 2 human_E3aI Consensus	6 mouse_E3αII 4 human_E3αII 15 mouse_E3αI 2 human_E3αI Consensus

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### Figure 1L

	•	·
1681 1681 1683 1675 1700	1731 1731 1733 1725 1725	٠.
I FLRVRECQV I FLRVRECQV I FLKI RECRV I FLKI RECRV	RKI QKL WQQH 1731 KKI QKL WHQH 1731 RKL HL VWQQH 1733 RKL HL VWQQH 1725 RKL HL VWQQH 1725	
LCLVCGSLLC SQSYCCQAEL EGEDVGACTA HTYSCGSGAG I FLRVRECQV 1681 LCLVCGSLLC SQSYCCQTEL EGEDVGACTA HTYSCGSGVG I FLRVRECQV 1681 LCLFCGAI LC SQNI CCQEI V NGEEVGACVF HALHCGAGVC I FLKI RECRV 1683 LCLFCGAI LC SQNI CCQEI V NGEEVGACI F HALHCGAGVC I FLKI RECRV 1675 LCLFCGAI LC SQNI CCQEI V NGEEVGACI F HALHCGAGVC I FLKI RECRV 1675 LCLFCGAI LC SQ CCQ GE. VGAC H CG. GV. I FL REC. V 1700	LFLAGKTKGC FYSPPYLDDY GETDQGLRRG NPLHLCQERF RKI QKLWQQH 1731 LFLAGKTKGC FYSPPYLDDY GETDQGLRRG NPLHLCKERF KKI QKLWHQH 1731 VLVEGKARGC AYPAPYLDEY GETDPGLKRG NPLHLSRERY RKLHLVWQQH 1733 VLVEGKARGC AYPAPYLDEY GETDPGLKRG NPLHLSRERY RKLHLVWQQH 1725	1755 1755 1757 1749
EGEDVGACTA EGEDVGACTA NGEEVGACVF NGEEVGACIF . GE. VGAC	GETDQGLRRG GETDQGLRRG GETDPGLKRG GETDPGLKRG GETD. GL. RG	
SQS YCCQAEL SQS YCCQTEL SQNI CCQEI V SQNI CCQEI V SQNI CCQEI V	FYSPPYLDDY FYSPPYLDDY AYPAPYLDEY AYPAPYLDEY .YPYLD.Y	TEEI GHAQ EANQTLVGI D WQHL FEI GHAQ EANQTLVGI D WQHL EEI ARSQ ETNOMLFGFN WQLL I EEI ARSQ ETNOMLFGFN WQLL EEIQ E. NQ. L.G. WQ. L.
LCLVCGSLLC LCLVCGSLLC LCLFCGAILC LCLFCGAILC LCLFCGAILC	LFLAGKTKGC LFLAGKTKGC VLVEGKARGC VLVEGKARGC	SITEEI GHAQ EANQTLVGI D WQHL SVTEEI GHAQ EANQTLVGI D WQHL CI I EEI ARSQ ETNQMLFGFN WQLL CI I EEI ARSQ ETNQMLFGFN WQLL . I . EEI Q E. NQ. L. G WQ. L.
mous e_E3αII huma n_E3αII mous e_E3αI huma n_E3αI Cons ens us	mous e_E3αII huma n_E3αII mous e_E3αI huma n_E3αI Cons ens us	mous e_E3aII huma n_E3aII mous e_E3aI huma n_E3aI Cons ens us
6 1 2 2	6 4 1 5 2 2	6 1 1 5 2

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### FIG. 2

### Tth Expression Profile of huE3 $\alpha$ -II in Human Tissues

Colon Thymus Spleen Kidney

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FIG. 3

### Tth Expression Profile of huE3 $\alpha$ -l in Human Tissues

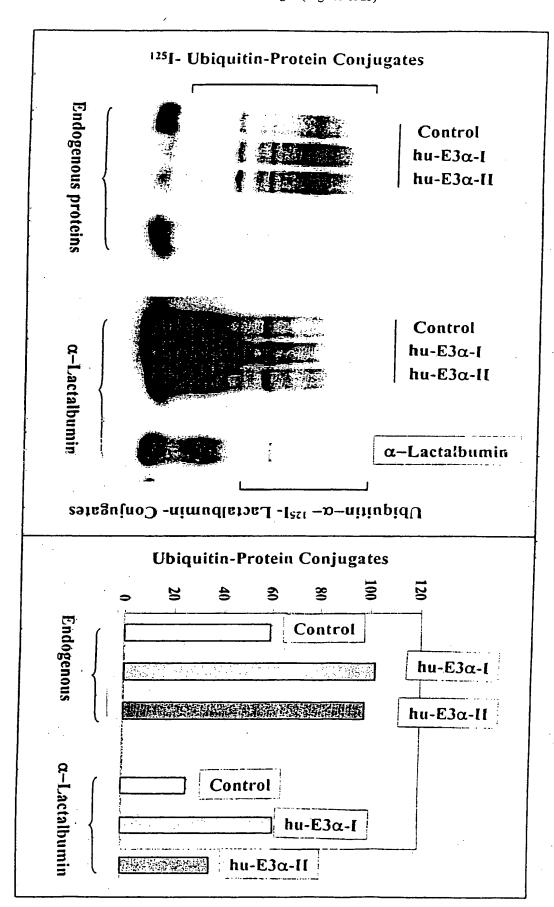
Heart Brain Placenta Lung Liver Skeletal Muscl Kidney

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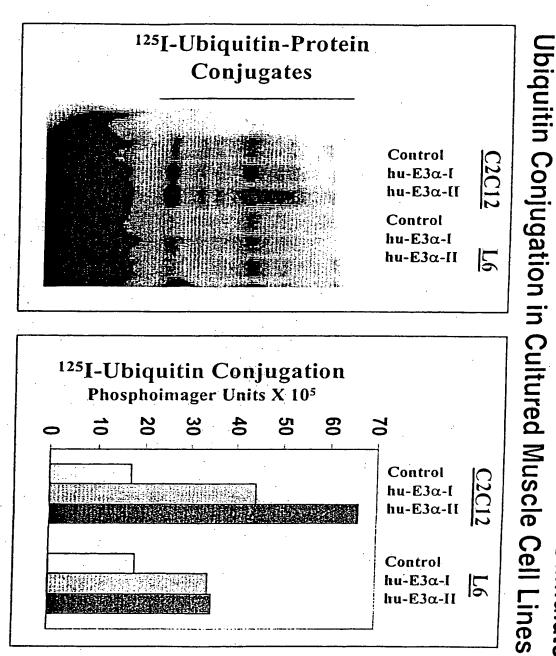
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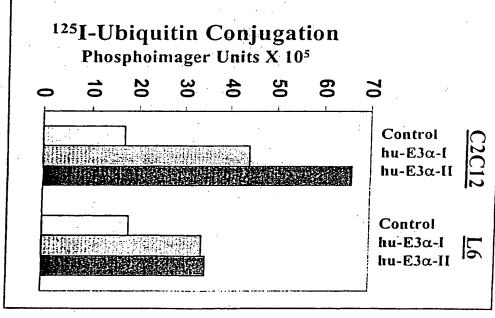
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Fig. 4 (Page 15 of 23)



# Ubiquitination of Endogenous Proteins

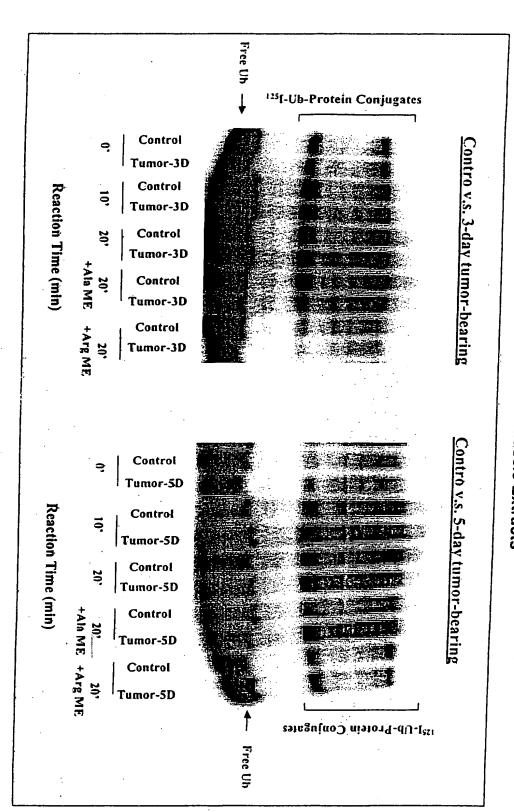




ansfection of Human E3a-I or E3a-II cDNA Stimulates

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## $^{125}$ l-Ubiquitin Conjugation to Muscle Proteins and Its Sensitivity to E3lpha Inhibitor in Skeletal Muscle Extracts

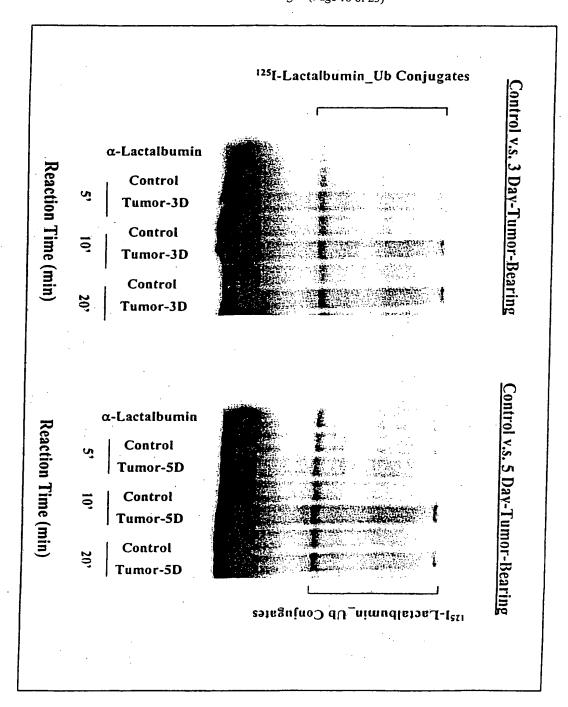


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Rates of Ubiquitination of N-end Rule Substrate

α-Lactalbumin in Skeletal Muscle Extracts

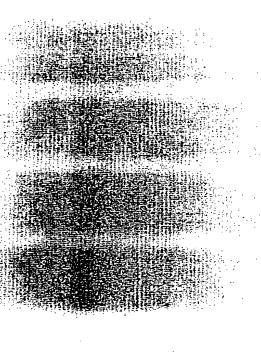
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# gastrocnemius muscles in YAH-130 exprimental cachexia model Northern blot analysis of E3lpha-I & E3lpha-II expression

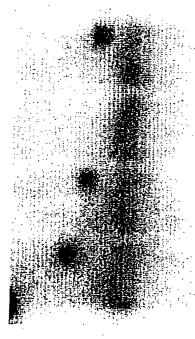
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Tumor, d3 Control, d5

Control, d3

Tumor, d5



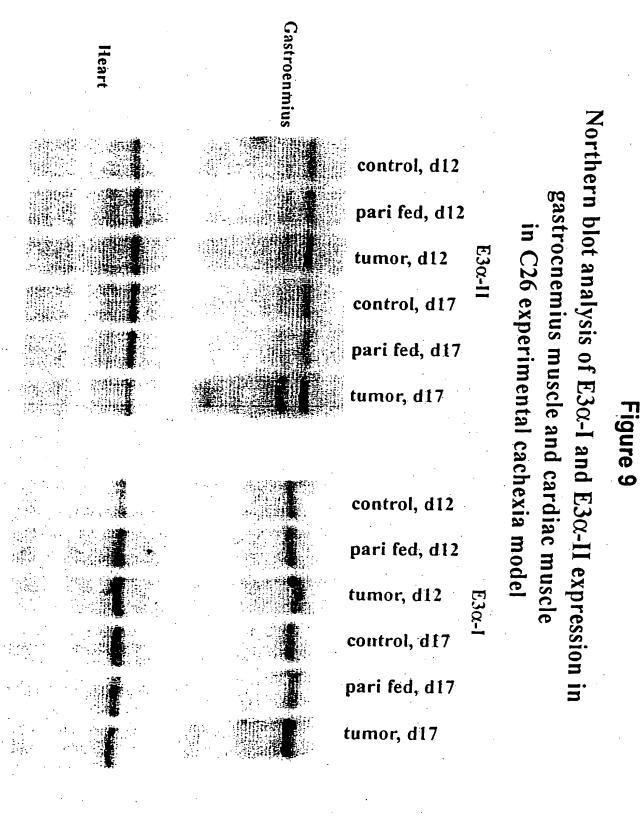
Control, d3

Tumor, d3

Control, d5

Tumor, d5

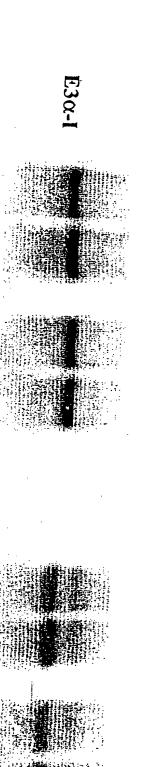
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Figure 10

induce E3lpha-II Expression in C2C12 myostube culture Proinflammatory cytokines TNF-lpha and IL-6 5 days



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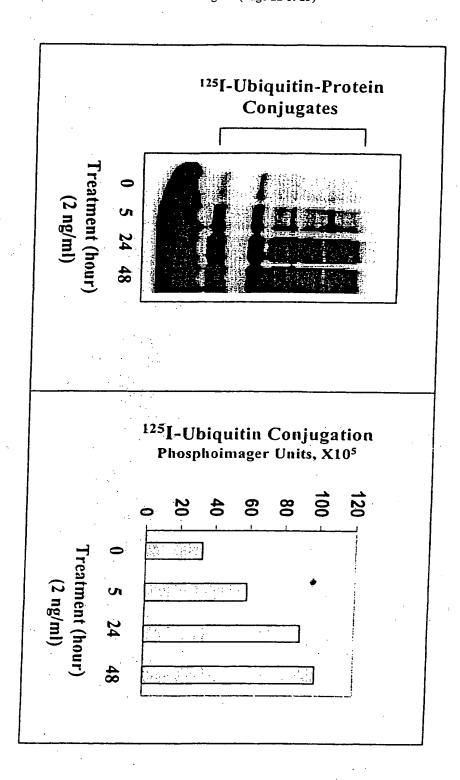
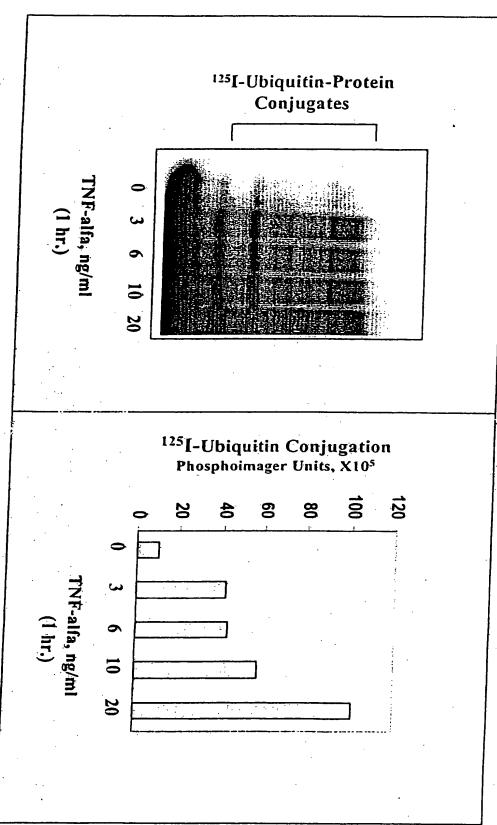


Figure 11

IL-6 Elicits Accelerated Ubiquitination in C2C12 Myotube Cultures



 ${\sf TNF}_{lpha}$  Elicits Accelerated Ubiquitination in C2C12 Myotube Cultures